Performing Iterative Non-blind Deconvolution with BiaQIm

Introduction

This is an extract from the BiaQIm User's Manual. More detail is given in chapter 11 of that manual where the background to the programs used in this example is explained (including basic information on how to use BiaQIm, the format of the deconvolution settings file and other step-by-step examples). Chapters and figures referred to in this text refer to the full BiaQIm User's manual which you can download from www.bialith.com (together with all the software).

The download installation package for BiaQIm includes a folder called 'DCTest' which contains the image files shown in this example so you can work along with it and do the deconvolution yourself.

Please remember that any image files you use with BiaQIm must not contain spaces in their name and must not be located on a path that contains spaces (such as 'My Documents' or anything in 'Documents and Settings'). This is because the external processes (such as deconvolution) are DOS-based programs that cannot handle such path names. If you install the BiaQIm package in the default location then you should be able to perform this example without problem.

Bear in mind also that your Windows system must be running in 'Windows Classic' mode if you have XP or Vista otherwise BiaQIm will not start. See the notes on the Software Download page of www.bialith.com for instructions on how to make your system change to 'Windows Classic' mode.

A step-by-step example

This step-by-step guide shows you how to perform Landweber deconvolution of a 128×128 pixel image in FITS format called 'BMoon.fit' by a 17×17 pixel PSF called 'PSF17.fit' which is also in FITS format. These are illustrated in figure 11.1 and both have pixels of double precision floating point numbers. It is important to ensure that both image and PSF have no negative valued pixels.
This is a very specific example for the purposes of illustrating the general method. Only a few of the many various options are used in this example.
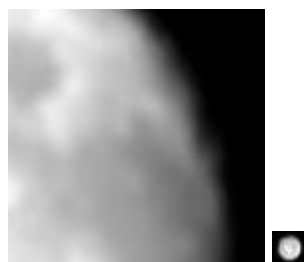

Figure 11.1 The input image (left) and PSF (right). The PSF is contrast stretched for the purposes of display.

Step 1: Load the input (blurred) image into BiaQIm
This can be done by simple drag-n-drop as described in chapter 2 (see the section entitled 'Loading an Image in Auto-Load Mode' and figure 2.4). See figure 11.2.

Step 2: Select the deconvolution external process in BiaQIm
How to do this was described in chapter 8. To recap, first go to the 'Process' tab of BiaQIm, then click the 'Choose' button and the process menu will appear. Move your mouse over the word 'Restoration' on the left to display the restoration submenu, then move your mouse across into the restoration submenu and left-click once on 'Iterative Non-Blind'. This will bring up the settings dialogue box for non-blind iterative deconvolution. See figure 11.3.
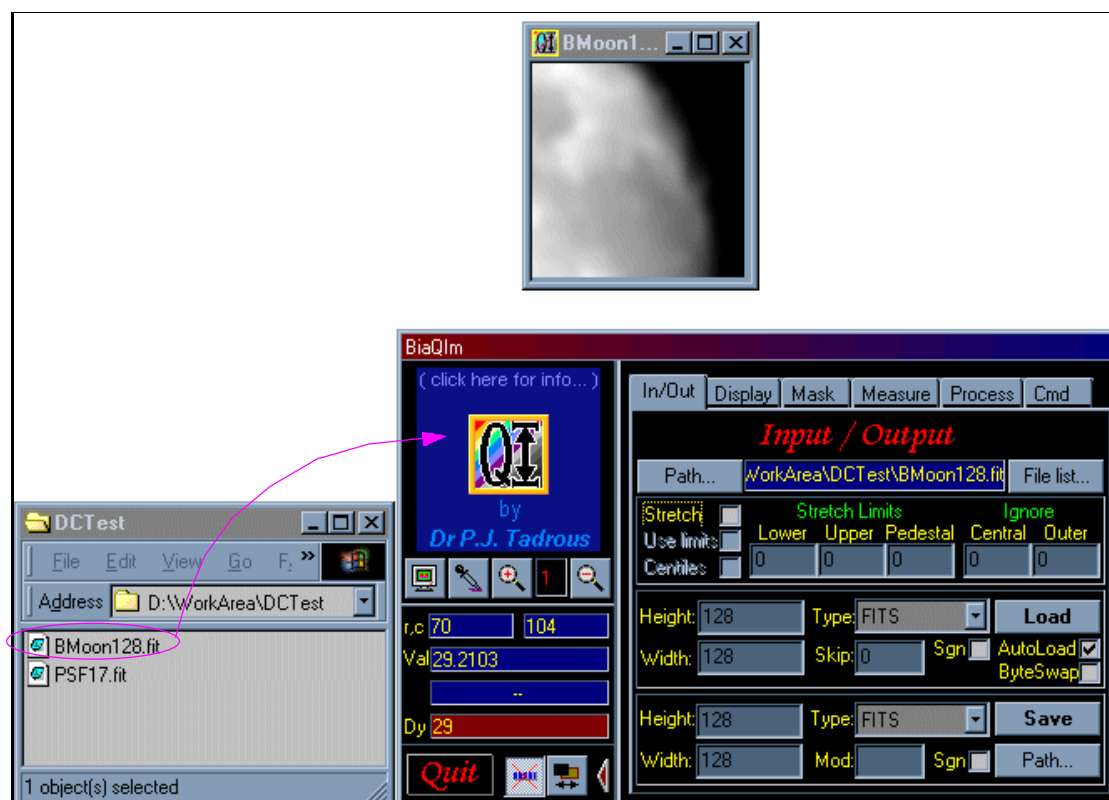
Figure 11.2 Drag the image 'BMoon.fit' and drop it into the 'QI' logo area of BiaQIm. The image will be displayed in the main display window.
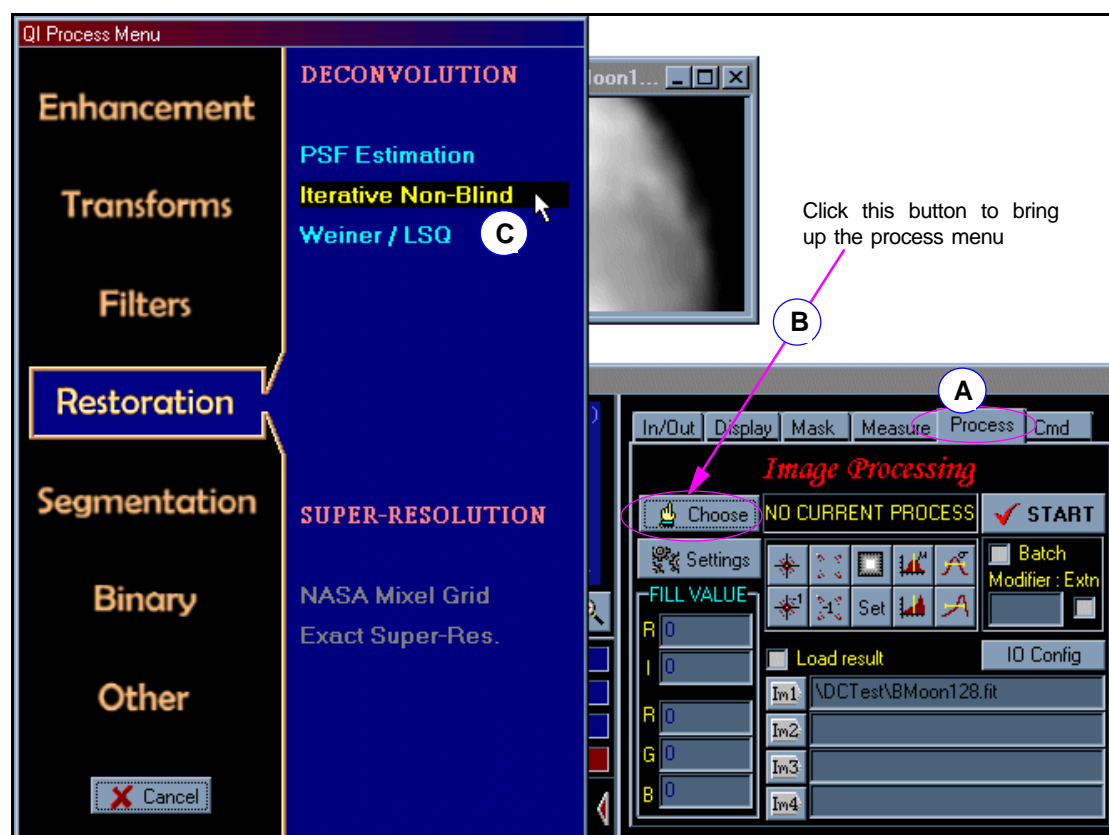

Figure 11.3 A) Select the 'Process' tab'. B) Click the 'Choose' button (circled) on the 'Process' tab of BiaQIm to bring up the process menu. C) Move your mouse over the word 'Restoration' on the left to bring up the restoration sub menu then move across to this sub-menu and select the 'Iterative Non-Blind' process (as shown). The process menu will disappear and the deconvolution settings dialogue will open up.

Step 3: Set the parameters via the settings dialogue box
The deconvolution settings dialogue box has a main tab section (at the very top) to select between the settings options for 'Iterative Non-Blind' deconvolution and the non-iterative 'Weiner / LSQ' settings. Because you selected 'Iterative Non-Blind' from the process menu in step 2, the deconvolution settings dialogue box will automatically open with the 'Iterative Non-Blind' tab selected for you. This has 5 sub-tabs of its own which we will work through one-by-one. In the following these will just be called 'tabs' and the settings for each of these 5 tabs are described in steps 3.1 to 3.5 below.

Step 3.1: The first tab (figure 11.4) allows you to select the deconvolution algorithm and type of convolution used in the algorithm (and boundary treatment in spatial convolution cases) using two drop down menus. You then have a series of text edit boxes to set the values for the convergence criteria (the 'CCRIT' values discussed in the section on settings files above) Only 3 of these boxes represent the actual convergence criteria, the two boxes on the right are for setting whether – and how often – you want intermediate results to be output (this feature will not be used in the present example so just ignore these boxes for now).
In this example, set the 'Algorithm' to 'Landweber LSQ' and leave the 'Convolution' at the default 'Fourier'. The only convergence criterion to set in this example is the 'Max itern' (maximum number of iterations) and set this to 4096 (you need to type this in the box. These settings are shown in figure 11.4.
Note that the settings options displayed may change depending on the convolution algorithm you select. For example if you selected 'Maxent 2 (Myrheim+Rue)' you would get four convergence criteria boxes (not 3) and these will be labelled according to the convergence criteria available for that algorithm. Other changes will occur in other tabs too according to the specific algorithm chosen at this stage.
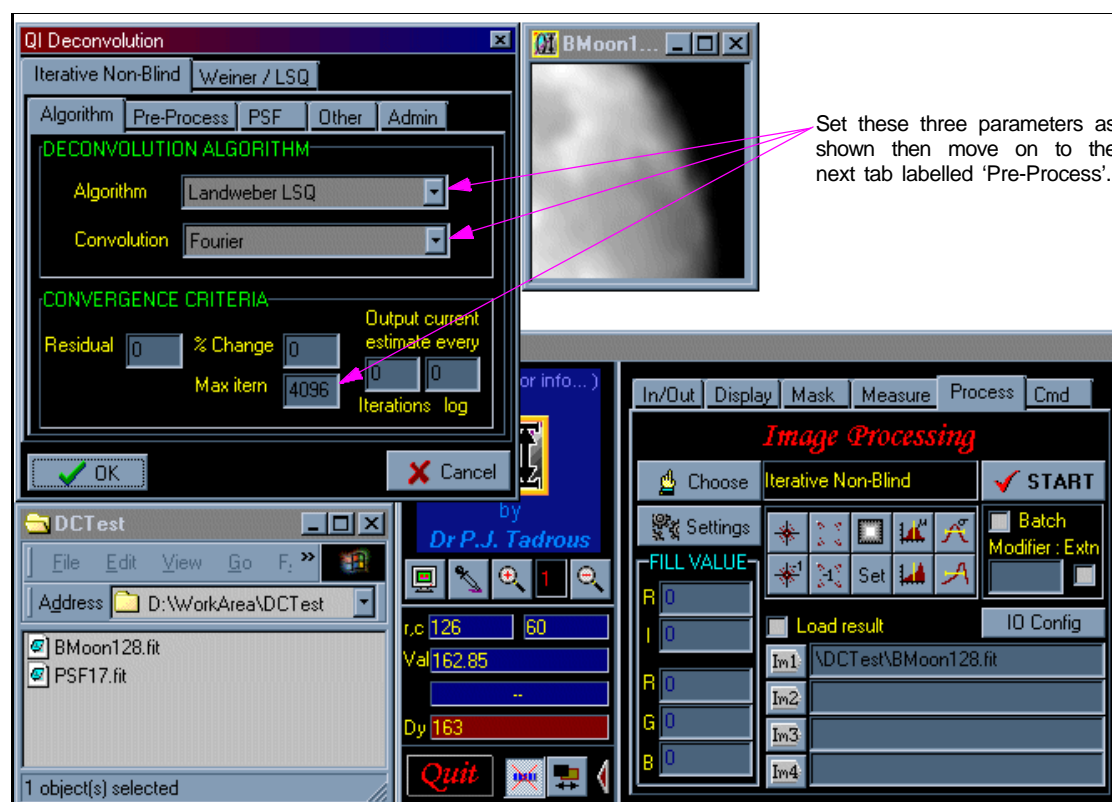

Figure 11.4 Select the appropriate settings for the deconvolution process: Algorithm, convolution type and convergence criteria.

Step 3.2: Now select the next tab along called 'Pre-Process' (figure 11.5 a) and tick the 'Solve' box at bottom right. This ensures that the SOLVE boundary method is used to avoid ringing from the sharp contrasts at the boundaries. The prior option should be left at 'Use input image as prior' because this usually gives the best results when using the SOLVE method. The other options are self-explanatory once you have read and understood the sections above on the settings files. Although not used in the present example, the method for using a custom prior file is explained below.

Using a prior file: To use a prior file you must tick the '**Use prior file ->**' box and then load the prior file to be used. This may be loaded by simple 'drag-n-drop' into this area (but the prior must be of the appropriate type and dimensions and if it is of a raw data type there must be an external header – .qih – file present in the same directory for drag-n-drop to succeed). Alternatively bring up a 'File Open' browser by a single left-click to the '**Prior …**' button and load the prior file that way. The '**Use Constant prior at value =**' tick box and edit box lets you specify a plain image (which is constructed internally) to use as prior where all pixels in that image have the same intensity value, namely the value you enter in the edit box. The '**Use MEAN as prior**' also constructs a plain prior image for you, this time with all its pixels set to the mean average intensity value of all pixels in the input image.

Step 3.3: Next go to the PSF tab and drag-n-drop the PSF file into the depressed rectangular space in the upper part of this window labelled with 'PSF File' in green (figure 11.5 b). This will load the PSF file and the PSF height and width will automatically be displayed. ensure that the 'Normalise' box is ticked (this is the default state of the box). An alternative way to load a PSF file is to bring up a 'File Open' browser by a single left click to the '**PSF file…**' button and load it this way.
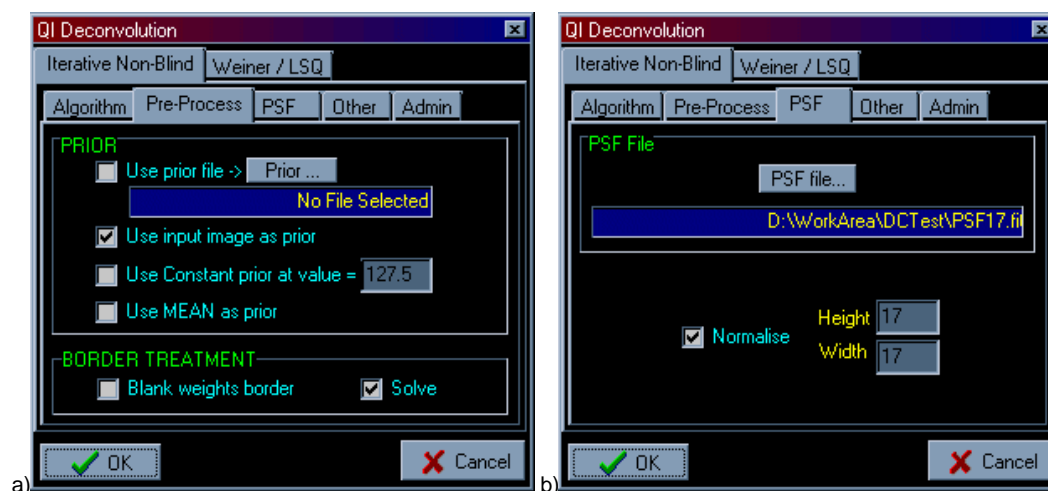

Figure 11.5 Select the appropriate settings for the deconvolution process: a) Preprocesses (priors and image border treatments - make sure you tick the 'SOLVE' box as shown) and b) PSF settings. If you simply 'drag-n-drop' the PSF file into the sunken area labelled 'PSF File' then it will automatically be loaded and the height and width displayed. Otherwise use the 'PSF file…' button to bring up a 'File Open' browser and load the PSF that way.
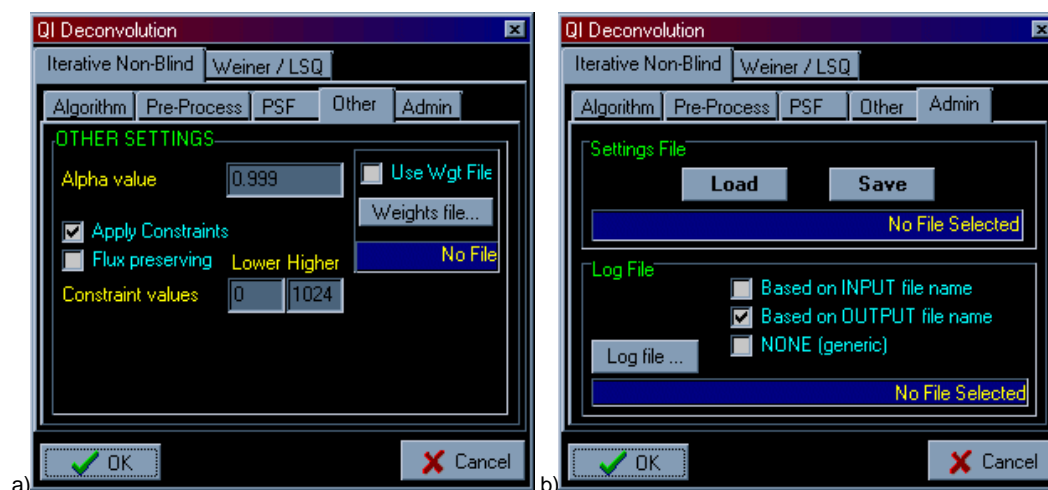

Figure 11.6 Select the appropriate settings for the deconvolution process: a) Other settings (various constants and constraints, weights files and masks) and b) Administrative settings (input and output files other than image-related files. These include the ability to save the settings file that BiaQIm will make for you using all your settings as well as load settings from a settings file you have on disk. It also include the log file options). If you have a settings file on disc then you can simply 'drag-n-drop' it into the sunken area labelled 'Settings File' and it will automatically set all the options in the dialogue boxes, tick boxes and drop-down menus in all the tabs according to the information contained in that settings file (you can also do this by clicking the 'Load' button and using a 'File Open' browser.

Step 3.4: Now go to the next tab along labelled 'Other' and ensure that the '**Alpha value**' text edit box contains the number 0.999. This is appropriate for most Landweber or Van Cittert deconvolutions but if you use maximum entropy (of Gull & Daniell) method then this box will change to being called '**Gamma value**' and you should generally set a lower value e.g. 0.01 or 0.005. The higher the gamma the faster the convergence but the maximum entropy (of Gull & Daniell) method will fail if this value is too large (it means that you have assumed there is too little noise in the image). For Lucy-Richardson or Super-resolution methods there is no alpha or gamma constant and so this box and its label will not be shown if you use those algorithms.

For our present example we will use constraints to ensure a non-negative solution (because the Landweber algorithm is a least squares method that does not have an inherent non-negativity constraint unlike Lucy-Richardson, Super-Resolution or maximum entropy methods which are all non-negatively constrained by design). Tick the '**Apply Constraints**' box and set the '**Lower**' box to 0 and the '**Higher**' box to some high number well above the maximum intensity level you would expect in the 'true' solution (in this example I use 1024).

The other available options for this tab will be described later but are not used in the current example.

Step 3.5: Finally select the 'Admin' tab and, in the section dealing with the log file settings in bottom half, tick the box labelled '**Based on OUTPUT' file name**' to ensure that the log file generated by the program has a name that is based on the resulting deconvolved image. You could alternatively use one of the other options or un-tick all these three boxes and select a custom file name by bringing up a browser dialogue box (via a single left-click to the '**Log file…**' button) and typing or selecting a name to use (clicking 'Save' on this browser dialogue just saves the file name you selected to BiaQIm, it does not save anything to disc).

If you want to, you may now save all the settings you have made over the last five steps by a single left-click to the '**Save**' button in the top half of this tab (the depressed area labelled 'Settings File' in green). This will bring up a 'File Save' dialogue box for you to select a name. The file will be saved in the appropriate format depending on which deconvolution algorithm you selected back at step 3.1. You may also load a settings file from disc. This can be done via the '**Load**' button (which brings up a 'File Open' dialogue box) or you may simply drag-n-drop a settings file into the depressed area. Either way, if you load a settings file (and it is of a valid format) then all the drop-down menus, tick boxes and edit boxes will automatically be set according to the settings in that file. This settings file load and save facility is a useful way of saving your settings from a previous deconvolution experiment so you can continue at a later date.

Before moving on to step 4, here is some information about settings not used in the current example but which have not yet been described.

Going back to the 'Other' tab (illustrated in figure 11.6 a) you will notice a depressed area in the top right of the window. This provides a facility to use a weights file (a raw array of doubles of same dimensions as the input image – described in the earlier sections dealing with the settings files). If you have such a file and you also have an external (.qih) header file present in the same directory, you may simply drag-n-drop the weights file into this depressed area and its file name and path will be recorded. You can also do this via a 'File Open' browser by a single left click to the '**Weights…**' button. However, recording the weights file name in this way is not sufficient for it to be used in the deconvolution. For that you must also tick the '**Use Wgt File**' box. The controls described in those tab are the same for the following deconvolution algorithms: Landweber, Van Cittert and Maximum entropy of Gull & Daniell (apart from the renaming of alpha to gamma in the latter).

For the Lucy-Richardson method the 'Other' tab changes its appearance to look like that shown in figure 11.7 a. In this case we do not have an 'alpha' or 'gamma' setting but instead there is a '**Background value**' edit box. Use this to specify the background grey level for a more accurate Lucy-Richardson deconvolution. This 'background' level is the lowest grey level anywhere in the 'true' solution. for astronomical images this can usually be set at zero (or the dark level if the images are not calibrated). For many brightfield images this will be non-zero. However, if you do not know what it should be you can usually get away with zero because no intensity level can be negative in any real world image that has been properly captured and calibrated. This 'Background value' setting is absent from the SuperResolution deconvolution algorithm version of the settings because it is not used in that algorithm.

For the Myrheim & Rue maximum entropy methods the 'Other' tab changes its appearance to look like that shown in figure 11.7 b. Here, the 'Alpha value' edit box is replaced by a '**Typical Noise Variance**' edit box and the constraints tick boxes are not available. Instead you have low and high thresholds on

the weights file (which correspond to the entries in the settings file called [VarThreshold_LH] and [Weight_set_LoHi] described above in the section on settings files). Another new setting is the '**Lowest value in p**' edit box corresponding to **[Minimum___Value]** which you must set to a number between 0 and 1 (usually close to 0). Notice also that there are now two depressed regions on the right of this tab. The top one (which is used for adding a weights file in the other methods) is now used to add an optional variance file in a similar way (you must tick the '**Use Var File**' box to actually use any variance file loaded into here). The lower depressed area operates in a similar manner but is used to add a weights mask (you must tick the '**Use Mask**' box to actually use any weights mask file loaded into here. Loading a variance file or weights mask is done via drag-n-drop or file browser (brought up by a single left click to the '**Variance file…**' or '**Weights Mask**' buttons).

Figure 11.7 a) The 'Other' tab settings for the Lucy-Richardson algorithm. b) The 'Other' tab settings for the Myrheim & Rue maximum entropy algorithms.

Another point of difference in the setting between Myrheim & Rue maximum entropy methods and the other algorithms is in the 'Pre-Process' tab. For Myrheim & Rue maximum entropy methods you will not get the options of using the SOLVE border treatment, neither can you set the prior image to a constant value of your choice or to the mean value of all the pixels in the input image (as you may with the other algorithms).

Step 4: Configure the inputs and outputs
Once you have finished defining all the settings click the 'OK' button on the settings dialogue box to confirm your settings choices – this is essential because the settings do not take effect until you click 'OK'. This window will close and the 'IO Configurator' window will appear (figure 11.8). Detail about the 'IO Configurator' is given in chapter 8 but for the purposes of this example, just set the output drop-down list to read 'Im2' and ensure that the input and output data types are both set to 'FITS' as shown in figure 11.8. Now close the window (Note: you do not have to close this window for the I/O settings to take effect. In many cases you may want to leave it open somewhere to ensure you always have the right input/output settings because these can change due to various actions you may take subsequently and selecting a new process causes some of these settings to return to default status).

Step 5: Run the process
Before you actually run it tick the 'Load result' box in the 'Process' tab of BiaQIm and enter a name for your resulting image in the edit box for 'Im2' such as 'LWMoon.fit' (see figure 11.9). Now left-click once on the 'START' button. Assuming you have the deconvolve.exe program on your PATH (or in the CWD) the process will start in a new DOS window that will open up automatically (figure 11.10). You will be able to monitor the progress of deconvolution as the current iteration and residual will be written out to the DOS prompt at each iteration and the 'best' result presented in brackets next to it. The 'best' (minimum residual) is usually the current iteration's value so this will change with every iteration – provided the solution is converging. If the solution begins to diverge then this minimum value will no longer be the current iteration's value and you will be able to see this in the DOS prompt.
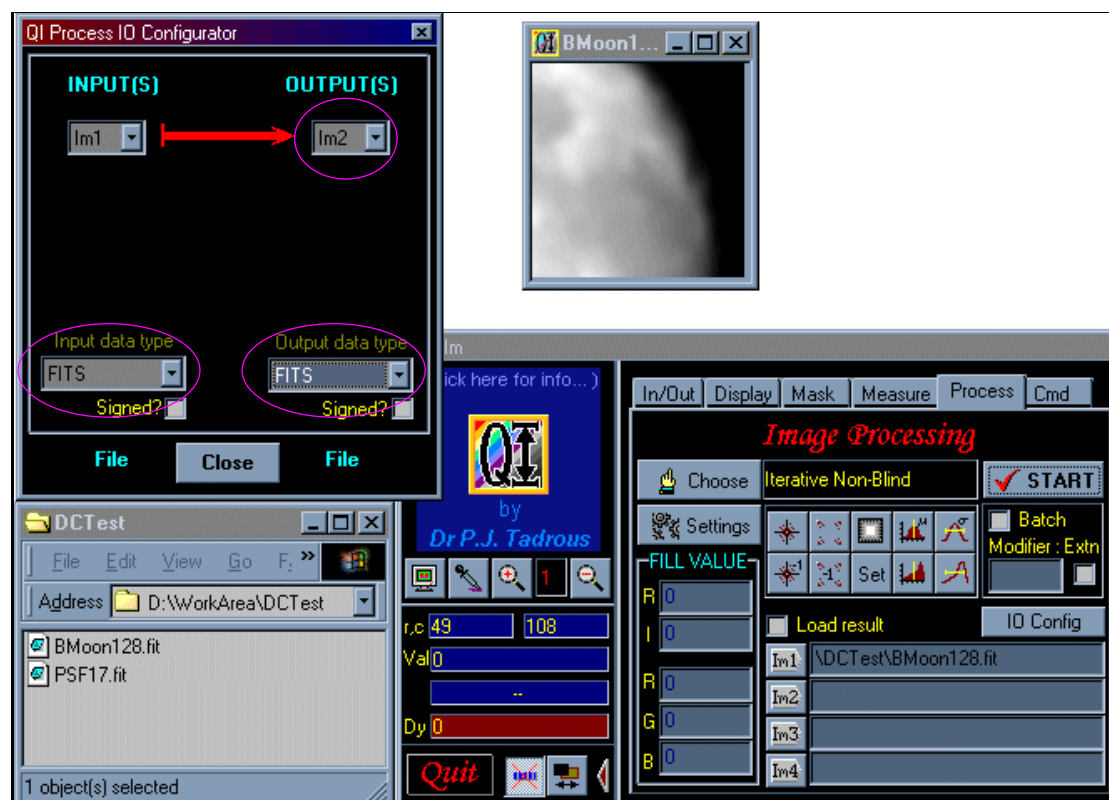
Figure 11.8 Set the options in the 'IO Configurator' window as shown in the figure (highlighted with ellipses).

Do the following in order:

1. Tick 'Load result'
2. Type the name of the output image in the edit box for 'Im2'. I have chosen to call it 'LWMoon.fit'
3. Left-click once the 'START' button.

These are shown highlighted by magenta ellipses.

Figure 11.9 Before finally running the process, first tick the 'Load result' box (so you will see the solution image as soon as the deconvolution program terminates) and type a name for the output image in the edit box labelled 'Im2'. In this example I use the name 'LWMoon.fit'. Now click the 'START' button and the program should begin to run in a new DOS window that will pop up for this purpose.
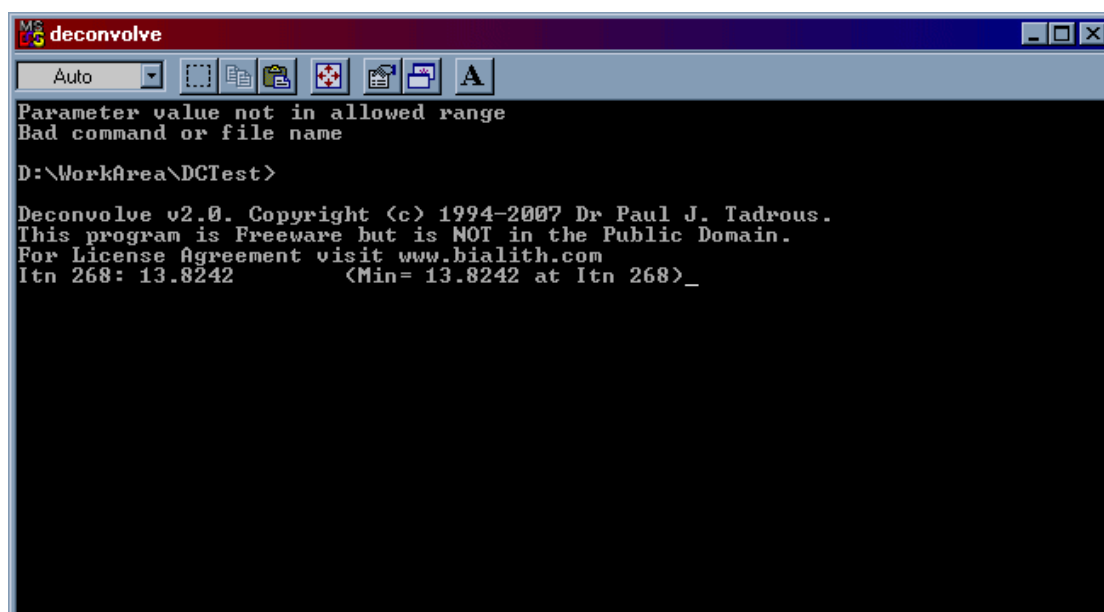
Figure 11.10 Once running the program will progress in a DOS window and BiaQIm will be unresponsive until the DOS window closes. The BiaQIm interface may not refresh if obscured during this time. This is normal. With deconvolution the output at the DOS prompt is updated with each iteration and tells you the current iteration, the values of the residual at this iteration and (in brackets) the iteration and value of the residual for the iteration that had the minimum residual value. If the solution is uniformly converging then this minimum value will always be the current iteration's value.
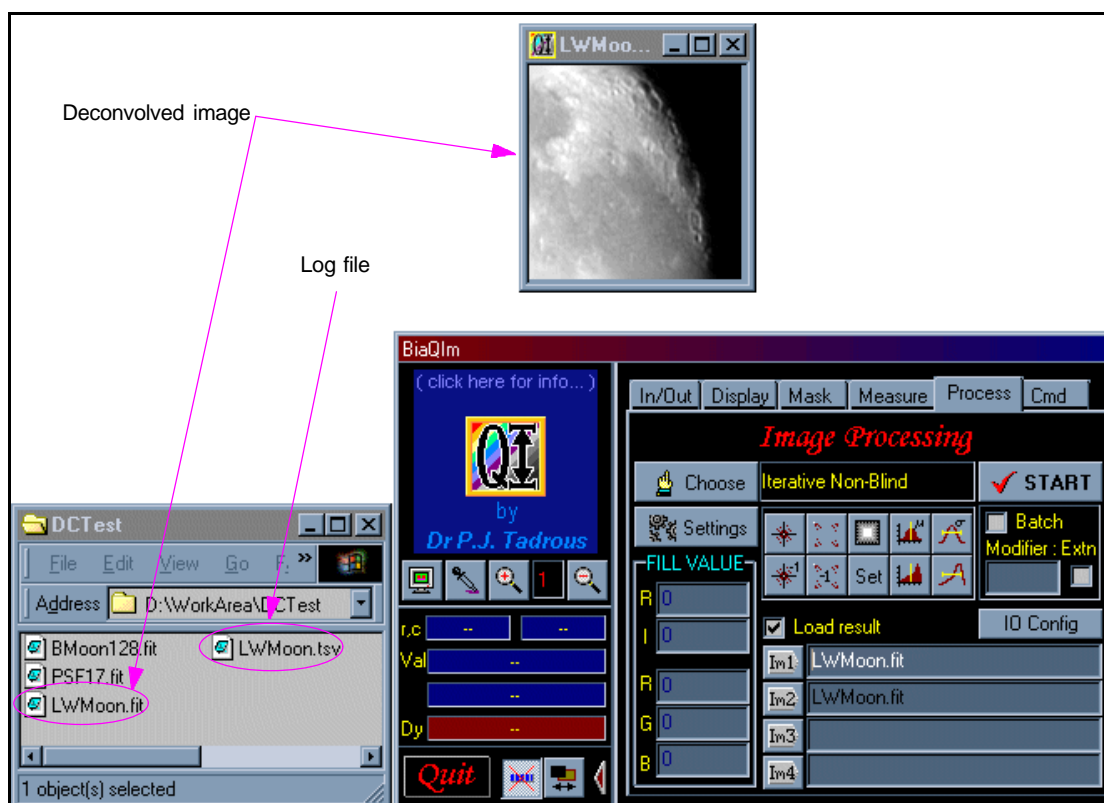

Figure 11.11 When finished the DOS box will close, the deconvolved image will automatically be loaded and displayed in the main display window of BiaQIm (because you ticked the 'load result' box earlier) and you will notice two new files in your folder. One is the resulting image file 'LWMoon.fit' and the other is the log file 'LWMoon.tsv'.

Making sense of the results

The result of performing this process is a deconvolved image called 'LWMoon.fit' and a log file called 'LWMoon.tsv' (figure 11.11).

The command line and settings

The command line constructed for you by BiaQIm can be seen on the 'Cmd' tab and will be this:

```
deconvolve.exe fits 128 128 1 D:\WorkArea\DCTest\BMoon128.fit  fits
LWMoon.fitC:\WINDOWS\Temp\QIdcs.txt
```

From this it can be seen that BiaQIm has created a temporary settings file for you called 'QIdcs.txt' in C:\WINDOWS\Temp\. You may read or copy this file (but as noted in step 3.5 above you can also save your own copy of this file via the 'Admin' tab of the deconvolution settings dialogue box.

The deconvolved image

The deconvolved image was produced by 4096 iterations of a constrained Landweber algorithm. Figure 11.12 compares this result with the result using the Maximum entropy method of Myrheim and Rue with a typical noise variance of 0.01 and only 1024 iterations. Boundary artefact problems appear greater in the latter but this is not necessarily a reflection of the technique's performance in general and it is inappropriate to go into details of deconvolution theory in this user's manual. Now that you are familiar with the controls you can experiment with various options.

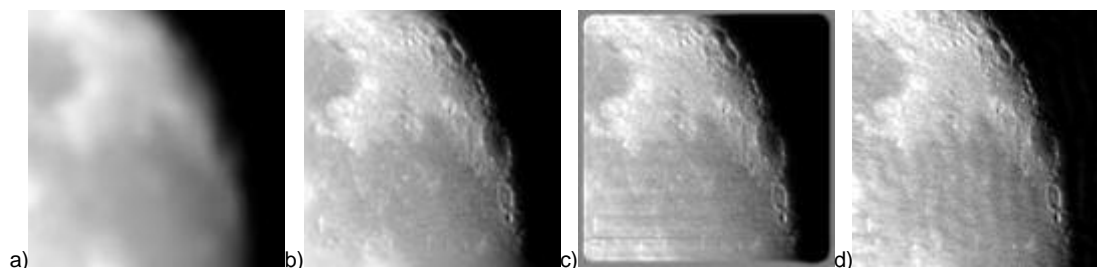a)   b)   c)   d)

Figure 11.12 Comparison of two deconvolution methods on the same input image (a) and PSF. b) Shows the result of the constrained Landweber method using 4096 iterations with an alpha of 0.999 and SOLVE border treatment. Note that this solution was still converging when stopped so further iterations could produce a higher degree of deconvolution but you would probably have to double the number of iterations each time to notice an improvement. c) Shows the result of 1024 iterations of Myrheim & Rue's maximum entropy with a typical noise variance of 0.01 and blanking of the weights border pixels. Both show a similar degree of deconvolution but boundary artefacts appear greater than in b). d) Shows the result of one-step (non-iterative) least squares deconvolution described in the second step-by-step example given in this chapter.

The log file and outputting intermediate results

The log file generated is a plain ASCII text file containing a record of the deconvolution settings used. In this record, a value of '-1' for a setting means that setting was not used in the deconvolution whilst a value of 1 or 0 in response to a question means 'YES' or 'NO' respectively. The log file also records the input image and PSF and the time it took to do the deconvolution.

The log file also records the residuals data at each iteration that is output as an intermediate result to disc during the deconvolution. In the current example the settings were such as to not allow output of intermediate results so only the final value of the residual is recorded in the settings file. However, if we repeat the procedure but this time, at step 3.1, we set the number '2' in the **Iterations** edit box and also in the '**log**' edit box (under 'Output current estimate every' in the bottom half of the 'Algorithm' tab of the deconvolution settings dialogue box – see figure 11.4) we will get a record of the residual (and an output of the current estimate as an image) at the second iteration, the 4th, the 8th, 16th, 32nd and so on. This will be accompanied by a .qfl file listing all the intermediate solution images that have been output so we can load this into BiaQIm and play the sequence as a movie or scroll through it. With regards to the data about the residuals at these intermediate point, they are stored in the log file in tsv format so you can plot a graph of the convergence behaviour using any graphing package that can handle tsv input (you may need to copy-paste this part of the log file into your graphing package's datasheet / spreadsheet rather than import the log file whole).